

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2001, 01:24:04 ; Search time 25.78 Seconds  
(without alignments)  
4854.724 Million cell updates/sec

Title: US-09-515-806-2

Perfect score: 1643

Sequence: 1 MAGRGAPGRGRDEPPESYP.....YNIKVEKKVSVLFLSYRDRD 1643

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	932	56.7	938	2 T46924	probable translation
2	14	0.9	1589	2 T13826	translation initia
3	11	0.7	576	2 S22127	protein kinase pol
4	10	0.6	307	2 S47244	C-raf protein - ze
5	10	0.6	312	2 T32446	hypothetical prote
6	10	0.6	323	1 TVMVF6	protein kinase (EC
7	10	0.6	328	1 TVMSBF	protein kinase B-r
8	10	0.6	380	1 TVFVYM	protein kinase (EC
9	10	0.6	437	1 TVMSRF	protein kinase A-r
10	10	0.6	450	1 TVFVMR	protein kinase (EC
11	10	0.6	462	2 S29851	protein kinase 6 (
12	10	0.6	547	2 S48441	K06H7.1 protein -
13	10	0.6	602	1 TVTRRR	protein kinase (EC
14	10	0.6	603	2 S34130	serine/threonine-s
15	10	0.6	603	2 A47545	protein kinase (EC
16	10	0.6	603	2 A54596	protein kinase A-r
17	10	0.6	604	1 S00726	protein kinase - m
18	10	0.6	606	1 TVHUAF	protein kinase A-r
19	10	0.6	615	2 T29223	hypothetical prote
20	10	0.6	638	1 TVXLRF	protein kinase raf
21	10	0.6	647	1 S00644	protein kinase raf
22	10	0.6	648	1 TVHUF6	protein kinase raf
23	10	0.6	648	1 TVTRTF	protein kinase raf
24	10	0.6	648	2 T43337	protein kinase raf
25	10	0.6	765	1 TVHUBF	polo-like kinase-1
26	10	0.6	781	1 TVFFDF	protein kinase B-r
27	10	0.6	806	1 JN0612	protein kinase Dra
28	10	0.6	807	1 I51153	protein kinase B-r
29	10	0.6	813	1 S33261	protein kinase lin

## ALIGNMENTS

RESULT 1

T46924

probable translation initiation factor eIF-2alpha kinase (EC 2.7.1.-) [similarity] -  
N/Alternate names: hypothetical protein DKFZp434P0612.1  
C/Species: Homo sapiens (man)

C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 20-Jun-2000

C/Accession: T46924; T46325

R/Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S.

submitted to the Protein Sequence Database, February 2000

A/Reference number: 224138

A/Accession: T46924

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-938 <AAA>

A/Cross-references: EMBL:AL157497

A/Experimental source: adult testis; clone DKFZp434F1312

R/Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A/Reference number: 223035

A/Accession: T46325

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 748-938 <AA2>

A/Cross-references: EMBL:AL137627

A/Experimental source: adult testis; clone DKFZp434P0612

C/Genetics:

A/Note: DKFZp434F1312.1; DKFZp434P0612.1

C/Superfamily: histidine--trNA ligase homology; protein kinase homology

C/Keywords: phosphotransferase

F.1-290/Domain: protein kinase homology (fragment) <KIN>

F.340-747/Domain: histidine--trNA ligase homology <HTL>

Query Match

Best Local Similarity 56.7%; Score 932; DB 2; Length 938;

Matches 932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 712 STSGERSASARPPATGPGSDDEDDDEHGCVFSQSFSPASDSSEDIIFNEDENSKSQ 771

Db 1 STSGERSASARPPATGPGSDDEDDDEHGCVFSQSFSPASDSSEDIIFNEDENSKSQ 60

QY 772 NQDECNKNCHESEPSVTTEAVHYLIQMEYCEKSTLRDTIDGGLYRDVRLWRLFRE 831

Db 61 NQDECNKNCHESEPSVTTEAVHYLIQMEYCEKSTLRDTIDGGLYRDVRLWRLFRE 120

QY 832 ILDLGAYIHEKGMIRDLKPVNIFLSDDHVKIGDFGLATDHLAFSADSKQDDQTGLIK 891

Db 121 ILDLGAYIHEKGMIRDLKPVNIFLSDDHVKIGDFGLATDHLAFSADSKQDDQTGLIK 180

QY 892 SDPSGHLTGMVGTALYVSPVQGGSTKSAYNOKVDLFLSLGIFFEMSYHPMVTASERFVL 951

Db 181 SDPSGHLTGMVGTALYVSPVQGGSTKSAYNOKVDLFLSLGIFFEMSYHPMVTASERFVL 240

30	10	0.6	1079	1	TVFVMI	gag-Rml1-env polyp
31	10	0.6	1696	2	T27447	hypothetical prote
32	9	0.5	294	1	DNCHEM	nucleophosmin - ch
33	9	0.5	303	2	A84831	probable protein k
34	9	0.5	399	2	T22168	hypothetical prote
35	9	0.5	402	1	TVFVUR	protein-tyrosine k
36	9	0.5	440	2	T25722	hypothetical prote
37	9	0.5	513	1	S50216	translation initia
38	9	0.5	515	1	A59309	translation initia
39	9	0.5	570	2	T37314	serine/threonine-s
40	9	0.5	607	2	S53387	autoantigen NOR-90
41	9	0.5	620	2	A53731	ribosomal transcri
42	9	0.5	626	2	A41284	
43	9	0.5	683	2	T38254	
44	9	0.5	727	2	S18193	
45	9	0.5	727	2	JC5113	

A:Cross-references: EMBL:AF056302; NID:g3046550; PID:g3046551; PIDN:AAC13490.1

C:Genetics:

A:Gene: GCN2

A:Cross-references: FlyBase:FBgn0019990

C:Superfamily: histidine--trna ligase homology; protein kinase homology

C:Keywords: phosphotransferase; protein kinase

F:521-898/Domain: protein kinase homology <KIN>

F:958-1285/Domain: histidine--trna ligase homology <HTL>

Query Match 0.9%; Score 14; DB 2; Length 1589;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 IHRDLKPVNIFLDS 858

Db 741 IHRDLKPVNIFLDS 754

RESULT 3

S22127

protein kinase poLo (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 24-Sep-1999

C:Accession: S22127

R:Sunkel, C.E.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22127

A:Accession: S22127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-576 <SUN>

A:Cross-references: EMBL:X63361; NID:g8355; PIDN:CAA44963.1; PID:g8356

C:Genetics:

A:Gene: FlyBase:poLo

A:Cross-references: FlyBase:FBgn0003124

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; phosphotransferase

F:23-277/Domain: protein kinase homology <KIN>

Query Match 0.7%; Score 11; DB 2; Length 576;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 HVKIGDFGLAT 871

Db 161 HVKIGDFGLAT 171

RESULT 4

S47244

C-rai protein - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 24-Sep-1999

C:Accession: S47244

R:Daniotti, J.L.

submitted to the EMBL Data Library, August 1994

A:Reference number: S47244

A:Accession: S47244

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-307 <DAN>

A:Cross-references: EMBL:X81128; NID:g534976; PIDN:CAA57035.1; PID:g534977

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP

F:7-273/Domain: protein kinase homology <KIN>

F:15-23/Region: protein kinase ATP-binding motif

Query Match 0.6%; Score 10; DB 2; Length 307;

Best Local Similarity 100.0%; Pred. No. 0.39;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 952 NQLRDPSPKFPEDDDGEHAKQSVISWLLNHDPAKRPATATELLKSELLPPQMESEL 1011

Db 241 NQLRDPSPKFPEDDDGEHAKQSVISWLLNHDPAKRPATATELLKSELLPPQMESEL 300

QY 1012 HEVLHPTLTNVGKAYRTMAQIFSORISPAIDYTVDSILKGNFISRTAKMOQHVCETI 1071

Db 301 HEVLHPTLTNVGKAYRTMAQIFSORISPAIDYTVDSILKGNFISRTAKMOQHVCETI 360

QY 1072 IRIFKRGAVQLCTPLLPNRROIYHEAALFMDHSGMLVLPDLRIPFARYVARNMI 1131

Db 361 IRIFKRGAVQLCTPLLPNRROIYHEAALFMDHSGMLVLPDLRIPFARYVARNMI 420

QY 1132 LNLKRYCIERVRPKLDRPHKLELCAFDIVTSTNSPLTAEIITTYIYIEIQEPAL 1191

Db 421 LNLKRYCIERVRPKLDRPHKLELCAFDIVTSTNSPLTAEIITTYIYIEIQEPAL 480

QY 1192 QERNYSIVLHNTMLLKAILHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSLSS 1251

Db 481 QERNYSIVLHNTMLLKAILHCGIPEDKLSQVYIILYDAVTEKLTREVEAKFCNLSLSS 540

QY 1252 NSLCRLYKFIEQKGLDQDLMPITNSLIKQKTGIAQLVKYGLKDEEVVGLLKLGLKQV 1311

Db 541 NSLCRLYKFIEQKGLDQDLMPITNSLIKQKTGIAQLVKYGLKDEEVVGLLKLGLKQV 600

QY 1312 LINLGLVYKVOOHNGIIFQVAFTRKRORAVPEILAAGRYDILLIPOFRGPQALGPVPTA 1371

Db 601 LINLGLVYKVOOHNGIIFQVAFTRKRORAVPEILAAGRYDILLIPOFRGPQALGPVPTA 660

QY 1372 IGVSTAIIDKISAAVNLNMEESVTISSCDLLVSVGOMSRRAINLTQKLTAGITAEIMYD 1431

Db 661 IGVSTAIIDKISAAVNLNMEESVTISSCDLLVSVGOMSRRAINLTQKLTAGITAEIMYD 720

QY 1432 WSQSOEELQECRHHETIYVALVSDKESGVKVSFPEKQTEKRVLETDLVHVLQKLR 1491

Db 721 WSQSOEELQECRHHETIYVALVSDKESGVKVSFPEKQTEKRVLETDLVHVLQKLR 780

QY 1492 TKVTDNRGRASDNLAVONLKGFSNAGLFEIHGATVVPVIVSVLAPEKLSASTRRYE 1551

Db 781 TKVTDNRGRASDNLAVONLKGFSNAGLFEIHGATVVPVIVSVLAPEKLSASTRRYE 840

QY 1552 TQVQTRLOTSLANLHOKSSEIEILAVDLPLKETILOFSLSEWDADQAFNTVKQLLSRLP 1611

Db 841 TQVQTRLOTSLANLHOKSSEIEILAVDLPLKETILOFSLSEWDADQAFNTVKQLLSRLP 900

QY 1612 KORYLKLVCDEIYNKVEKVSFLYSYRDD 1643

Db 901 KORYLKLVCDEIYNKVEKVSFLYSYRDD 932

RESULT 2

T13826

translation initiation factor eIF-2 alpha kinase (EC 2.7.1.1) [imported] - fruit fly (D

C:Species: Drosophila melanogaster

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000

C:Accession: T13826; T13060

R:Sanjoto, J.; Alcald, J.; Mendez, R.; Pulido, D.; de Haro, C.

J. Biol. Chem. 272, 12544-12550, 1997

A:Title: Cloning and characterization of a cDNA encoding a protein synthesis initiation

A:Reference number: 217783; MUID:97284729

A:Accession: T13826

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1589 <SAN>

A:Cross-references: EMBL:U80223; NID:g2073563; PID:g2073564; PIDN:AAC47516.1

R:Olson, D.S.; Jordan, B.; Chen, D.; Wek, R.C.; Cavanaugh, D.R.

Genetics 149, 1495-1509, 1998

A:Title: Isolation of the gene encoding the Drosophila melanogaster homolog of the Sacch

A:Reference number: 213099; MUID:98315111

A:Accession: T13060

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-687, 'K', 689-1426, 'H', 1428-1589 <OLS>

QY 862 VKIGDFGLAT 871  
 Db 142 VKIGDFGLAT 151

## RESULT 5

T32446  
 hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 03-Nov-2000  
 C:Accession: T32446  
 R:Maggi, L.; Harper, M.  
 submitted to the EMBL Data Library, September 1997  
 A:Description: The sequence of C. elegans cosmid H42K12.  
 A:Reference number: 221169  
 A:Accession: T32446  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-312 <MAG>  
 A:Cross-references: EMBL:AF026207; PIDN:AAB71265.1; GSPDB:GN00028; CESP:H42K12.1  
 A:Experimental source: strain Bristol N2; clone H42K12  
 C:Genetics:  
 A:Gene: CESP:H42K12.1  
 A:Map position: X  
 A:Introns: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 0.6%; Score 10; DB 2; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 902 VGTALYVSPE 911  
 Db 177 VGTALYVSPE 186

## RESULT 6

TVMVF6  
 protein kinase (EC 2.7.1.37) raf - murine sarcoma virus 3611  
 N:Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-s  
 C:Species: murine sarcoma virus 3611  
 A:Note: host Mus musculus (mouse)  
 C>Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 23-Feb-1997  
 C:Accession: A00638; A38020  
 R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.  
 Science 223, 813-816, 1984  
 A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by murin  
 A:Reference number: A00638; MUID:84121298  
 A:Accession: A00638  
 A:Molecule type: DNA  
 A:Residues: 1-323 <KAN>  
 A:Experimental source: ATCC 45010  
 R:Mark, G.E.; Rapp, U.R.  
 Science 224, 285-289, 1984  
 A:Title: Primary structure of v-raf: relatedness to the src family of oncogenes.  
 A:Reference number: A38020; MUID:84172180  
 A:Accession: A38020  
 A:Molecule type: DNA  
 A:Residues: 1-323 <MAR>  
 C:Comment: This protein is translated as a gag-raf polypeptide.  
 C:Genetics:  
 A:Gene: raf  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase;  
 F:22-288/Domain: protein kinase homology <KIN>  
 F:30-38/Region: protein kinase ATP-binding motif  
 F:50/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 0.41;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 Db 157 VKIGDFGLAT 166

## RESULT 7

TVMSEF  
 protein kinase B-raf (EC 2.7.1.1) - mouse (fragment)  
 N:Alternate names: Kinase-related transforming protein B-raf; P94  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1993 #sequence\_revision 09-Aug-1996 #text\_change 23-Feb-1997  
 C:Accession: A40951  
 R:Miki, T.; Fleming, T.P.; Crescenzi, M.; Molloy, C.J.; Blam, S.B.; Reynolds, S.H.; A  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5167-5171, 1991  
 A:Title: Development of a highly efficient expression cDNA cloning system: applicatio  
 A:Reference number: A40951; MUID:91271351  
 A:Accession: A40951  
 A:Molecule type: mRNA  
 A:Residues: 1-328 <MIK>  
 A:Cross-references: GB:M64429  
 A:Note: the reported sequence is the product of recombination of TIF1 and B-raf genes  
 C:Genetics:  
 A:Gene: B-raf  
 C:Function:  
 A:Description: member of signal transduction pathway(s) activated by nerve growth fac  
 A:Pathway: MAP kinase cascade  
 A:Note: found in hippocampal neurons and dendritic spines and in high levels in fetal  
 C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; p  
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncog  
 F:17-283/Domain: protein kinase homology <KIN>  
 F:25-33/Region: protein kinase ATP-binding motif  
 F:45/Active site: Lys #status predicted  
 F:169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 Db 152 VKIGDFGLAT 161

## RESULT 8

TVMVM  
 protein kinase (EC 2.7.1.37) ml - avian myelocytomatosis virus MH2  
 N:Alternate names: kinase-related transforming protein ml (mht); ml proto-oncogene  
 C:Species: avian myelocytomatosis virus MH2  
 A:Note: host Gallus gallus (chicken)  
 C>Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 23-Feb-1997  
 C:Accession: A00639; B00638; A21137  
 R:Sutrave, P.; Bonner, T.I.; Rapp, U.R.; Jansen, H.W.; Patschinsky, T.; Blister, K.  
 Nature 309, 85-88, 1984  
 A:Title: Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine  
 A:Reference number: A00639; MUID:84191511  
 A:Accession: A00639  
 A:Molecule type: DNA  
 A:Residues: 1-380 <SUT>  
 A:Cross-references: GB:K02082  
 A:Note: the authors translated the codon CAG for residue 58 as Gly  
 R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.  
 Science 223, 813-816, 1984  
 A:Title: A common onc gene sequence transduced by avian carcinoma virus MH2 and by mu  
 A:Reference number: A00638; MUID:84121298  
 A:Accession: B00638  
 A:Molecule type: DNA  
 A:Residues: 1-210, 'E', 212-380 <KAN>  
 A:Cross-references: GB:K02084  
 R:Kan, N.C.; Flordellis, C.S.; Mark, G.E.; Duesberg, P.H.; Papas, T.S.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3000-3004, 1984

A:Title: Nucleotide sequence of avian carcinoma virus MH2: two potential onc genes, one  
 A:Reference number: A21137; MUID:84221892  
 A:Accession: A21137  
 A:Molecule type: DNA  
 A:Residues: 1-210,'E',212-230,'E',232-380 <KA2>  
 A:Cross-references: GB:K02082  
 C:Comment: This protein is translated as a gag-mht or gag-mil polyprotein.  
 C:Genetics:  
 A:Gene: mht; mil  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: Atp; oncogene; phosphotransferase; polyprotein; serine/threonine-specific pr  
 F:80-346/Domain: protein kinase homology <KIN>  
 F:88-96/Region: protein kinase ATP-binding motif  
 F:108/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 0.47;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 Db 215 VKIGDFGLAT 224

## RESULT 9

TMMSRF  
 N:protein kinase A-raf-1 (EC 2.7.1.1) - mouse (fragment)  
 N:Alternate names: A-raf-1 proto-oncogene protein-serine/threonine kinase; kinase-relate  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 11-Jun-1999  
 C:Accession: A25382  
 R:Huleihel, M.; Goldsbrough, M.; Cleveland, J.; Gunnell, M.; Bonner, T.; Rapp, U.R.  
 Mol. Cell. Biol. 6, 2655-2662, 1986  
 A:Title: Characterization of murine A-raf, a new oncogene related to the v-raf oncogene.  
 A:Reference number: A25382; MUID:87064566  
 A:Accession: A25382  
 A:Molecule type: mRNA  
 A:Residues: 1-437 <HUL>  
 A:Cross-references: GB:M13071; NID:gi92016; PIDN:AAA37258.1; PID:g387104  
 C:Genetics:  
 A:Gene: A-raf  
 C:Function:  
 A:Description: signal transduction between cell membrane and nucleus; after phosphorylat  
 A:Pathway: MAP kinase cascade  
 A:Note: in mouse, expressed in urogenital tissues and, at lower levels, in other tissues  
 C:Superfamily: protein kinase A-raf; protein kinase C zinc-binding repeat homology; prot  
 C:Keywords: Atp; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
 F:139-405/Domain: protein kinase homology <KIN>  
 F:147-155/Region: protein kinase ATP-binding motif  
 F:47/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:56/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted  
 F:167/Active site: Lys #status predicted  
 F:413/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 0.53;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 Db 274 VKIGDFGLAT 283

## RESULT 10

TFVWVR  
 N:protein kinase (EC 2.7.1.37) R-mil - Rous-associated virus (type 1)  
 N:Alternate names: kinase-related transforming protein R-mil; R-mil proto-oncogene prote  
 C:Species: Rous-associated virus  
 A:Note: host Gallus gallus (chicken)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 11-Jun-1999  
 C:Accession: A40341

R:Felder, M.P.; Eychene, A.; Barnier, J.V.; Calogeraki, I.; Calothy, G.; Marx, M.  
 J. Virol. 65, 3633-3640, 1991  
 A:Title: Common mechanism of retrovirus activation and transduction of c-mil and c-Rm  
 A:Reference number: A40341; MUID:91251215  
 A:Accession: A40341  
 A:Molecule type: DNA  
 A:Residues: 1-450 <FEU>  
 A:Cross-references: GB:MG2407; NID:g210080; PIDN:AAA42549.1; PID:g210081  
 C:Comment: This protein is translated as a mil-env polyprotein.  
 C:Genetics:  
 A:Gene: R-mil  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: Atp; oncogene; phosphotransferase; serine/threonine-specific protein kina  
 F:81-347/Domain: protein kinase homology <KIN>  
 F:89-97/Region: protein kinase ATP-binding motif  
 F:109/Active site: Lys #status predicted

Query Match 0.6%; Score 10; DB 1; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 0.54;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 Db 216 VKIGDFGLAT 225

## RESULT 11

S29851  
 N:protein kinase 6 (EC 2.7.1.1) - soybean  
 C:Species: Glycine max (soybean)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
 C:Accession: S29851; S27760  
 R:Feng, X.H.; Zhao, Y.; Bottino, P.J.; Kung, S.  
 Biochim. Biophys. Acta 1172, 200-204, 1993  
 A:Title: Cloning and characterization of a novel member of protein kinase family from  
 A:Reference number: S29851; MUID:93176812  
 A:Accession: S29851  
 A:Molecule type: mRNA  
 A:Residues: 1-462 <FEN>  
 A:Cross-references: EMBL:M67449; NID:q170046; PIDN:AAA34002.1; PID:q170047  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
 C:Keywords: Atp; phosphotransferase  
 F:154-419/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 0.56;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 636 EVTLRLHH 645  
 |||||  
 Db 207 EVTLRLHH 216

## RESULT 12

S44841  
 N:K06H7.1 protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
 C:Accession: S44841  
 R:Favella, A.D.  
 submitted to the EMBL Data Library, May 1993  
 A:Description: Sequence of the C. elegans cosmid K06H7.  
 A:Reference number: S44620  
 A:Accession: S44841  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-547 <FAV>  
 A:Cross-references: EMBL:L15314; NID:g289690; PIDN:AAA28084.1; PID:g289691  
 C:Genetics:  
 A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C;Keywords: ATP; serine/threonine-specific protein kinase  
F;265-518/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 547;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
|||||  
Db 404 VKIGDFGLAT 413

## RESULT 13

TVTRRR  
protein kinase (EC 2.7.1.37) raf - rat  
N;Alternate names: kinase-related transforming protein raf; raf proto-oncogene protein-  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 11-Jun-1999

C;Accession: B26126  
R;Ishikawa, F.; Takaku, F.; Nagao, M.; Sugimura, T.  
Mol. Cell. Biol. 7, 1226-1232, 1987  
A;Title: Rat c-raf oncogene activation by a rearrangement that produces a fused protein.  
A;Reference number: A26126; MUID:87117291  
A;Accession: B26126  
A;Molecule type: mRNA  
A;Residues: 1-602 <ISH>  
A;Cross-references: GB:M15428; NID:g206546; PIDN:AAAA2002.1; PID:g206547  
C;Genetics:

A;Gene: raf  
C;Superfamily: rat protein kinase raf; protein kinase homology  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine  
F;301-567/Domain: protein kinase homology <KIN>  
F;309-317/Region: protein kinase ATP-binding motif  
F;329/Active site: Lys status predicted  
F;453/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 0.6%; Score 10; DB 1; Length 602;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
|||||  
Db 436 VKIGDFGLAT 445

## RESULT 14

S34130  
serine/threonine-specific protein kinase PLK (EC 2.7.1.-) - human  
N;Alternate names: polo-like protein kinase; protein kinase plk-1  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-Sep-1999  
C;Accession: S34130; I38123; S61543  
R;Golsteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.  
submitted to the EMBL Data Library, June 1993  
A;Description: Cloning and characterization of a novel human protein kinase plk-1 a pote  
hrough mitosis.

A;Reference number: S34130  
A;Accession: S34130  
A;Molecule type: mRNA  
A;Residues: 1-603 <COL>  
A;Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51837.1; PID:g312998  
A;Experimental source: nasopharyngeal carcinoma  
R;Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.; St  
proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994  
A;Title: Induction and down-regulation of PLK, a human serine/threonine kinase expressed  
A;Reference number: A53134; MUID:94173904  
A;Accession: I38123  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>  
A;Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769

A;Experimental source: lung tumor  
R;Brauninger, A.; Strehardt, K.; Ruebsamen-Waigmann, H.

Oncogene 11, 1793-1800, 1995  
A;Title: Identification and functional characterization of the human and murine polo-  
A;Reference number: S61543; MUID:96068906

A;Accession: S61543  
A;Molecule type: DNA  
A;Residues: 1-122, 'T', 124-136 <BRA>  
A;Cross-references: EMBL:X90725; NID:g1061143; PIDN:CAA62260.1; PID:g1061144  
A;Experimental source: placenta  
A;Note: the authors translated the codon AGC for residue 107 as Met  
C;Genetics:

A;Gene: GDB:PLK  
A;Cross-references: GDB:331003

A;Map position: 1pter-17p12  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F;51-305/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 603;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
|||||  
Db 190 VKIGDFGLAT 199

## RESULT 15

A47545

protein kinase (EC 2.7.1.37) plk - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999  
C;Accession: A47545  
R;Clay, F.J.; McEwen, S.J.; Bertonecello, I.; Wilks, A.F.; Dunn, A.R.  
Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993  
A;Title: Identification and cloning of a protein kinase-encoding mouse gene, Plk, rel  
A;Reference number: A47545; MUID:93281660

A;Accession: A47545  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-603 <CLA>

A;Cross-references: GB:L06144; NID:g309461; PIDN:AAA39948.1; PID:g309462  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
C;Keywords: ATP; phosphotransferase  
F;51-305/Domain: protein kinase homology <KIN>

Query Match 0.6%; Score 10; DB 2; Length 603;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
|||||  
Db 190 VKIGDFGLAT 199

Search completed: October 22, 2001, 01:28:08  
Job time: 244 sec

Mon Oct 22 08:29:39 2001

us-09-515-806-2.rpr

---

Page 6